FIG. 1A

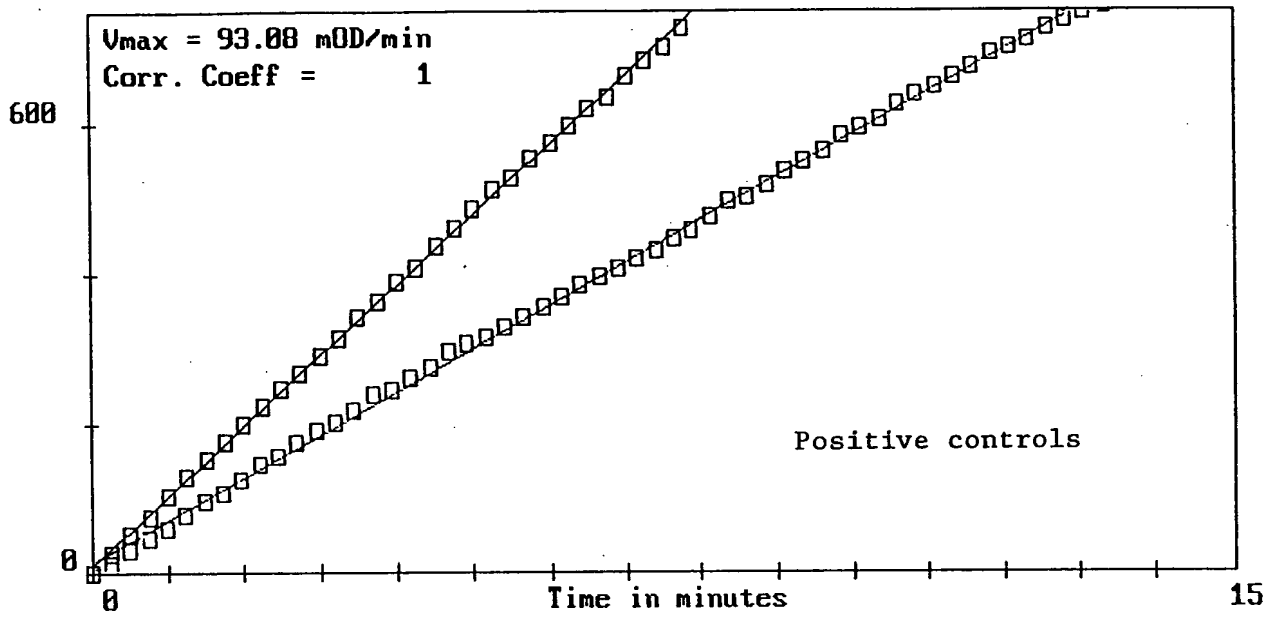

Vmax = 93.08 mOD/min
Corr. Coeff = 1
600
0
Positive controls
0
Time in minutes
15

FIG. 1B

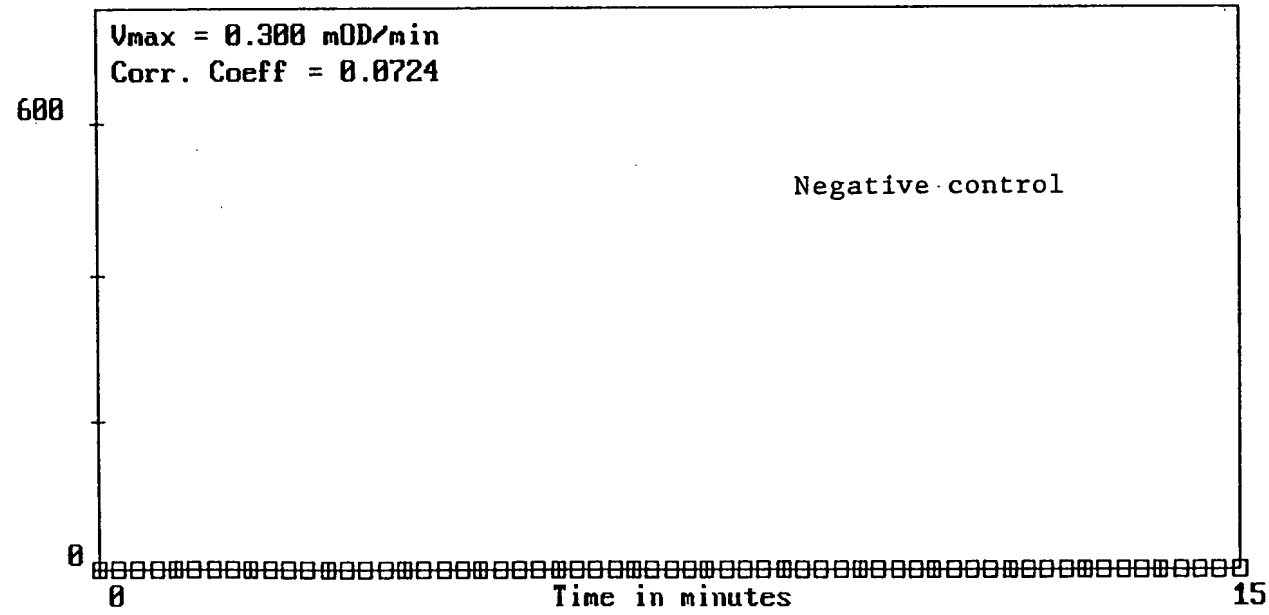

Vmax = 0.300 mOD/min
Corr. Coeff = 0.0724
600
0
Negative control
0
Time in minutes
15

FIG. 1C

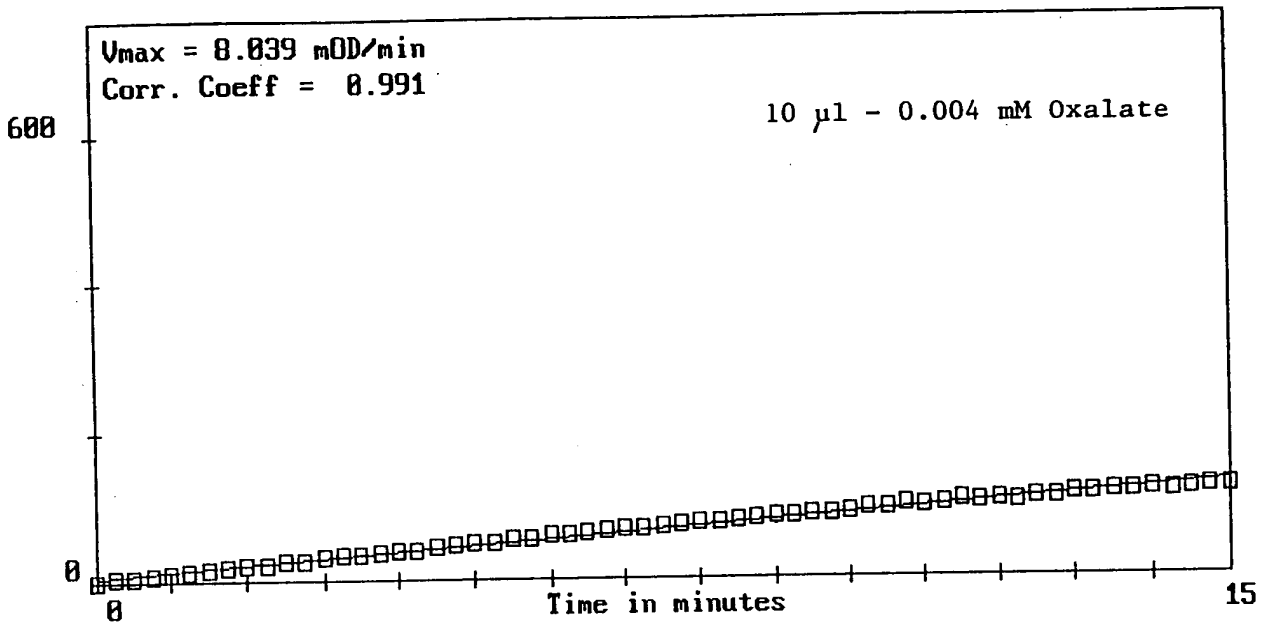

Vmax = 8.039 mOD/min
Corr. Coeff = 0.991
10 µl - 0.004 mM Oxalate
600
0
0
Time in minutes
15

FIG. 1D

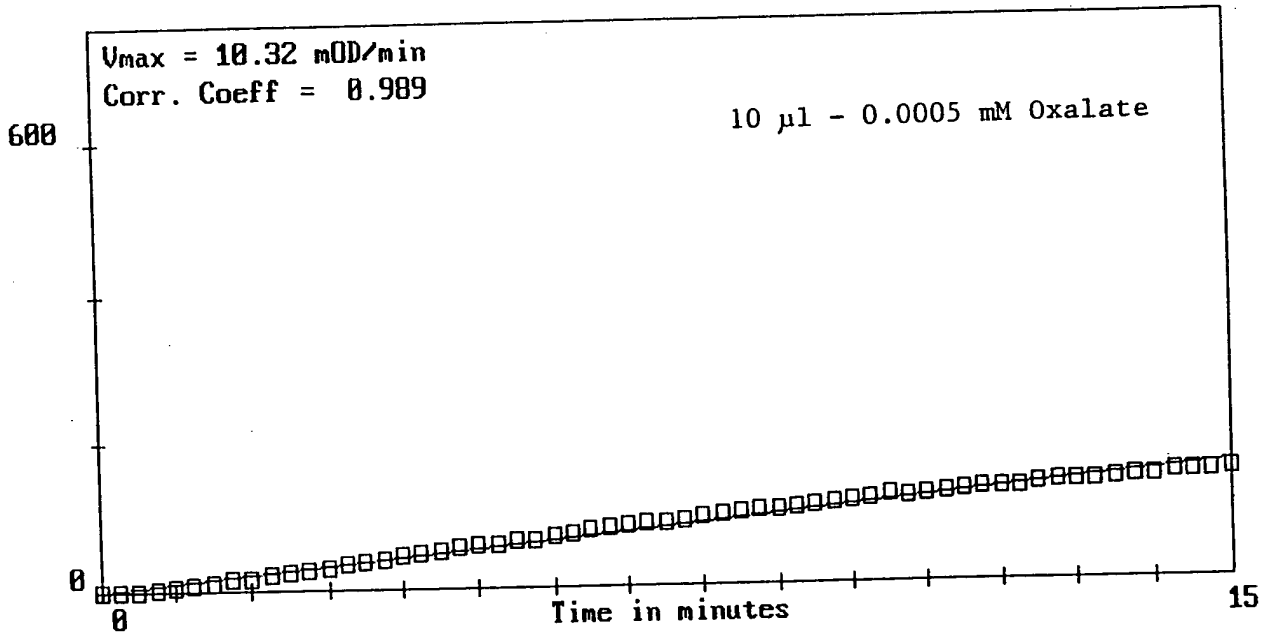

Vmax = 10.32 mOD/min
Corr. Coeff = 0.989
10 µl - 0.0005 mM Oxalate
600
0
0
Time in minutes
15

FIG. 1E

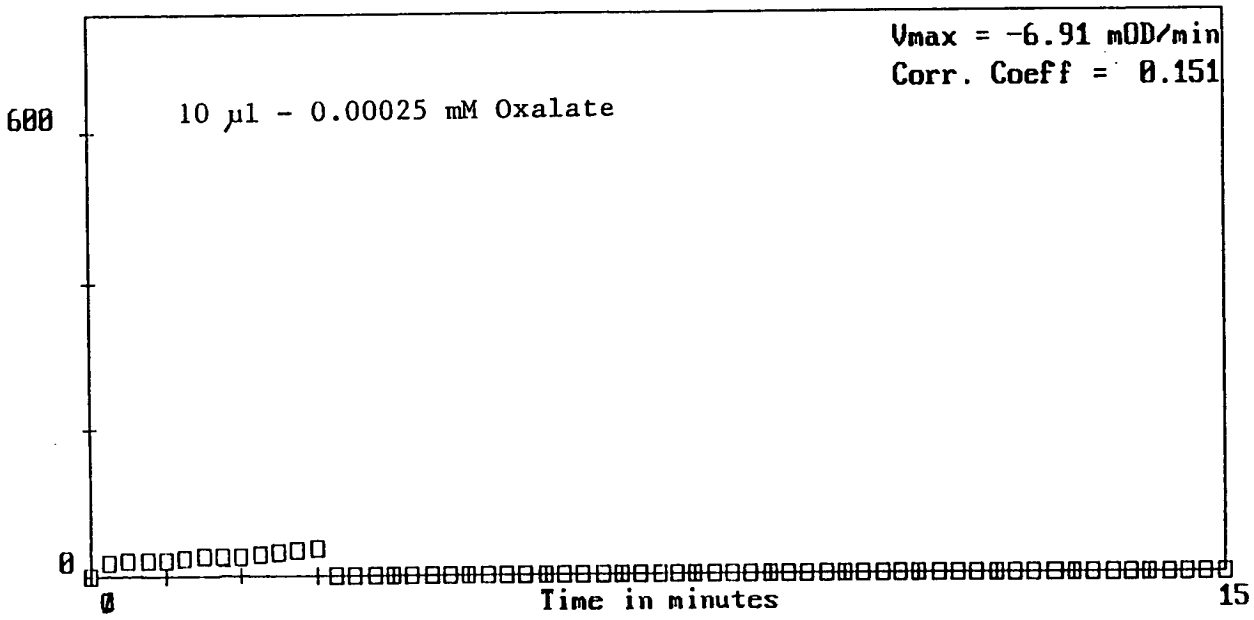

Vmax = -6.91 mOD/min
Corr. Coeff = 0.151
600
10 µl - 0.00025 mM Oxalate
0
0
Time in minutes
15

FIG. 2A

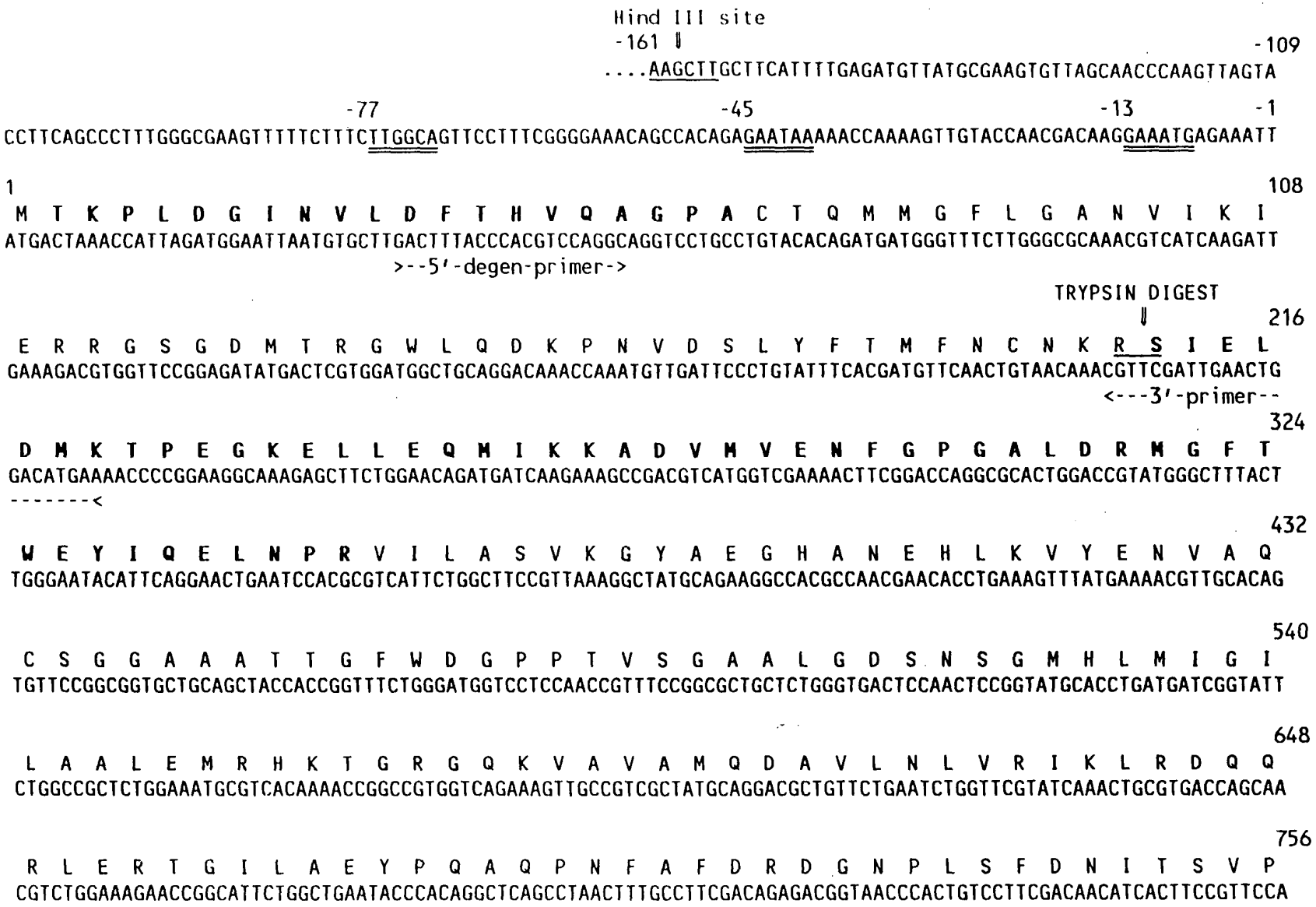

Hind III site
-161
-109
....AAGCTTGCTTCATTTTGAGATGTTATGCGAAGTGTTAGCAACCCAAGTTAGTA
-77
-45
-13
-1
CCTTCAGCCCTTTGGGCGAAGTTTTTCTTTCTTGGCAGTTCCTTTCGGGGAAACAGCCACAGAGAATAAAAACCAAAAGTTGTACCAACGACAAGGAAATGAGAAATT
1
108
M T K P L D G I N V L D F T H V Q A G P A C T Q M M G F L G A N V I K I
ATGACTAAACCATTAGATGGAATTAATGTGCTTGACTTTACCCACGTCCAGGCAGGTCCTGCCTGTACACAGATGATGGGTTTCTTGGGCGCAAACGTCATCAAGATT
>--5'-degen-primer->
TRYPSIN DIGEST
216
E R R G S G D M T R G W L Q D K P N V D S L Y F T M F N C N K R S I E L
GAAAGACGTGGTTCCGGAGATATGACTCGTGGATGGCTGCAGGACAAACCAAATGTTGATTCCCTGTATTTCACGATGTTCAACTGTAACAAACGTTCGATTGAACTG
<---3'-primer--
324
D M K T P E G K E L L E Q M I K K A D V M V E N F G P G A L D R M G F T
GACATGAAAACCCCGGAAGGCAAAGAGCTTCTGGAACAGATGATCAAGAAAGCCGACGTCATGGTCGAAAACTTCGGACCAGGCGCACTGGACCGTATGGGCTTTACT
-------<
432
W E Y I Q E L N P R V I L A S V K G Y A E G H A N E H L K V Y E N V A Q
TGGGAATACATTCAGGAACTGAATCCACGCGTCATTCTGGCTTCCGTTAAAGGCTATGCAGAAGGCCACGCCAACGAACACCTGAAAGTTTATGAAAACGTTGCACAG
540
C S G G A A A T T G F W D G P P T V S G A A L G D S N S G M H L M I G I
TGTTCCGGCGGTGCTGCAGCTACCACCGGTTTCTGGGATGGTCCTCCAACCGTTTCCGGCGCTGCTCTGGGTGACTCCAACTCCGGTATGCACCTGATGATCGGTATT
648
L A A L E M R H K T G R G Q K V A V A M Q D A V L N L V R I K L R D Q Q
CTGGCCGCTCTGGAAATGCGTCACAAAACCGGCCGTGGTCAGAAAGTTGCCGTCGCTATGCAGGACGCTGTTCTGAATCTGGTTCGTATCAAACTGCGTGACCAGCAA
756
R L E R T G I L A E Y P Q A Q P N F A F D R D G N P L S F D N I T S V P
CGTCTGGAAAGAACCGGCATTCTGGCTGAATACCCACAGGCTCAGCCTAACTTTGCCTTCGACAGAGACGGTAACCCACTGTCCTTCGACAACATCACTTCCGTTCCA

FIG. 2B

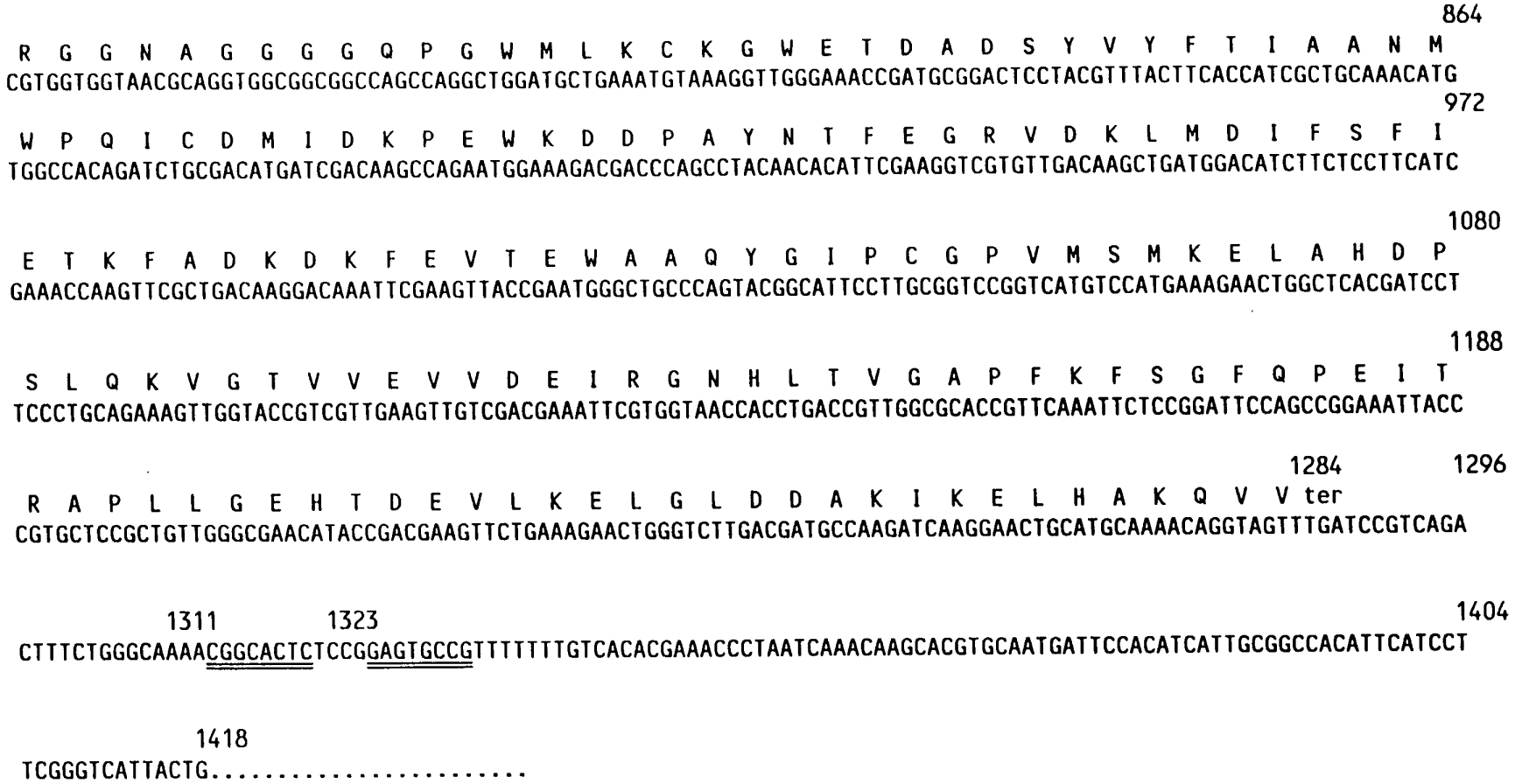

864
R G G N A G G G G Q P G W M L K C K G W E T D A D S Y V Y F T I A A N M
CGTGGTGGTAACGCAGGTGGCGGCGGCCAGCCAGGCTGGATGCTGAAATGTAAAGGTTGGGAAACCGATGCGGACTCCTACGTTTACTTCACCATCGCTGCAAACATG
972
W P Q I C D M I D K P E W K D D P A Y N T F E G R V D K L M D I F S F I
TGGCCACAGATCTGCGACATGATCGACAAGCCAGAATGGAAAGACGACCCAGCCTACAACACATTCGAAGGTCGTGTTGACAAGCTGATGGACATCTTCTCCTTCATC
1080
E T K F A D K D K F E V T E W A A Q Y G I P C G P V M S M K E L A H D P
GAAACCAAGTTCGCTGACAAGGACAAATTCGAAGTTACCGAATGGGCTGCCCAGTACGGCATTCCTTGCGGTCCGGTCATGTCCATGAAAGAACTGGCTCACGATCCT
1188
S L Q K V G T V V E V V D E I R G N H L T V G A P F K F S G F Q P E I T
TCCCTGCAGAAAGTTGGTACCGTCGTTGAAGTTGTCGACGAAATTCGTGGTAACCACCTGACCGTTGGCGCACCGTTCAAATTCTCCGGATTCCAGCCGGAAATTACC
1284
1296
R A P L L G E H T D E V L K E L G L D D A K I K E L H A K Q V V ter
CGTGCTCCGCTGTTGGGCGAACATACCGACGAAGTTCTGAAAGAACTGGGTCTTGACGATGCCAAGATCAAGGAACTGCATGCAAAACAGGTAGTTTGATCCGTCAGA
1311
1323
1404
CTTTCTGGGCAAAACGGCACTCTCCGGAGTGCCGTTTTTTTGTCACACGAAACCCTAATCAAACAAGCACGTGCAATGATTCCACATCATTGCGGCCACATTCATCCT
1418
TCGGGTCATTACTG.....

FIG. 3A

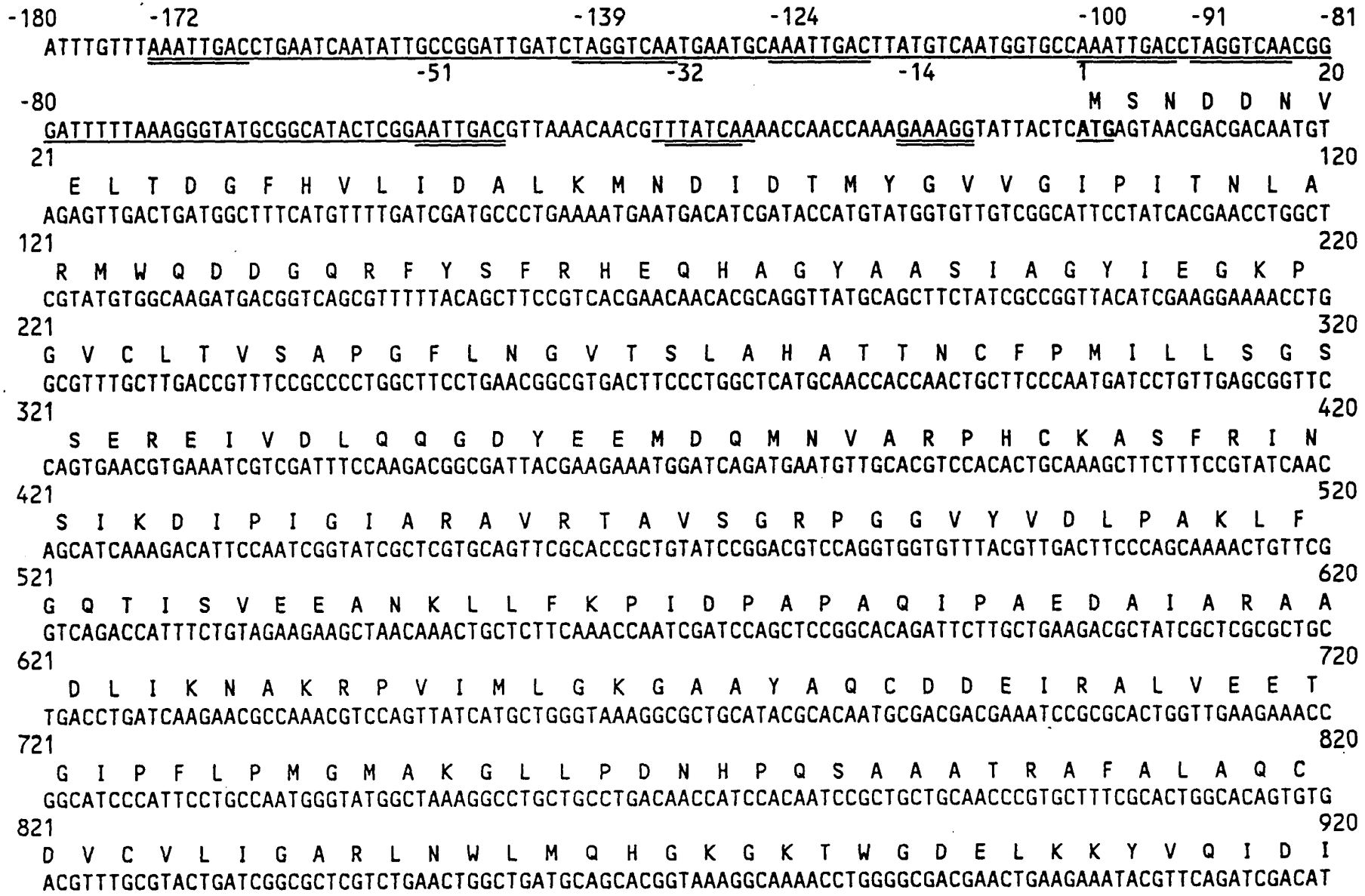
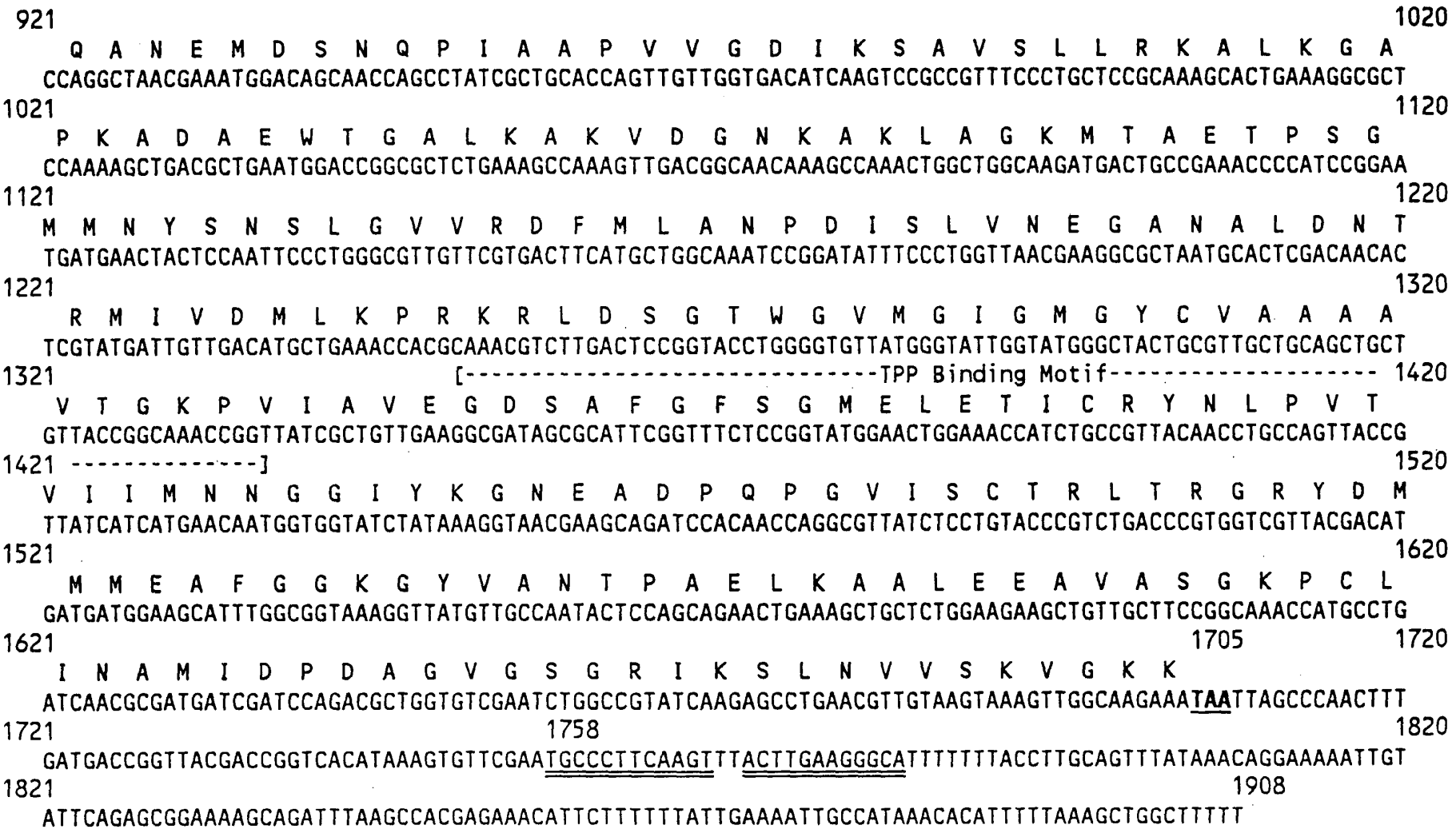

-180 -172 -139 -124 -100 -91 -81
ATTTGTTTAAATTGACCTGAATCAATATTGCCGGATTGATCTAGGTCAATGAATGCAAATTGACTTATGTCAATGGTGCCAAATTGACCTAGGTCAACGG
-51 -32 -14 1 20
-80 M S N D D N V
GATTTTTAAAGGGTATGCGGCATACTCGGAATTGACGTTAAACAACGTTTATCAAAACCAACCAAAGAAAGGTATTACTCATGAGTAACGACGACAATGT
21 120
E L T D G F H V L I D A L K M N D I D T M Y G V V G I P I T N L A
AGAGTTGACTGATGGCTTTCATGTTTTGATCGATGCCCTGAAAATGAATGACATCGATACCATGTATGGTGTTGTCGGCATTCCTATCACGAACCTGGCT
121 220
R M W Q D D G Q R F Y S F R H E Q H A G Y A A S I A G Y I E G K P
CGTATGTGGCAAGATGACGGTCAGCGTTTTTACAGCTTCCGTCACGAACAACACGCAGGTTATGCAGCTTCTATCGCCGGTTACATCGAAGGAAAACCTG
221 320
G V C L T V S A P G F L N G V T S L A H A T T N C F P M I L L S G S
GCGTTTGCTTGACCGTTTCCGCCCCTGGCTTCCTGAACGGCGTGACTTCCCTGGCTCATGCAACCACCAACTGCTTCCCAATGATCCTGTTGAGCGGTTC
321 420
S E R E I V D L Q Q G D Y E E M D Q M N V A R P H C K A S F R I N
CAGTGAACGTGAAATCGTCGATTTCCAAGACGGCGATTACGAAGAAATGGATCAGATGAATGTTGCACGTCCACACTGCAAAGCTTCTTTCCGTATCAAC
421 520
S I K D I P I G I A R A V R T A V S G R P G G V Y V D L P A K L F
AGCATCAAAGACATTCCAATCGGTATCGCTCGTGCAGTTCGCACCGCTGTATCCGGACGTCCAGGTGGTGTTTACGTTGACTTCCCAGCAAAACTGTTCG
521 620
G Q T I S V E E A N K L L F K P I D P A P A Q I P A E D A I A R A A
GTCAGACCATTTCTGTAGAAGAAGCTAACAAACTGCTCTTCAAACCAATCGATCCAGCTCCGGCACAGATTCTTGCTGAAGACGCTATCGCTCGCGCTGC
621 720
D L I K N A K R P V I M L G K G A A Y A Q C D D E I R A L V E E T
TGACCTGATCAAGAACGCCAAACGTCCAGTTATCATGCTGGGTAAAGGCGCTGCATACGCACAATGCGACGACGAAATCCGCGCACTGGTTGAAGAAACC
721 820
G I P F L P M G M A K G L L P D N H P Q S A A A T R A F A L A Q C
GGCATCCCATTCCTGCCAATGGGTATGGCTAAAGGCCTGCTGCCTGACAACCATCCACAATCCGCTGCTGCAACCCGTGCTTTCGCACTGGCACAGTGTG
821 920
D V C V L I G A R L N W L M Q H G K G K T W G D E L K K Y V Q I D I
ACGTTTGCGTACTGATCGGCGCTCGTCTGAACTGGCTGATGCAGCACGGTAAAGGCAAAACCTGGGGCGACGAACTGAAGAAATACGTTCAGATCGACAT

FIG. 3B


921
1020
Q A N E M D S N Q P I A A P V V G D I K S A V S L L R K A L K G A
CCAGGCTAACGAAATGGACAGCAACCAGCCTATCGCTGCACCAGTTGTTGGTGACATCAAGTCCGCCGTTTCCCTGCTCCGCAAAGCACTGAAAGGCGCT
1021
1120
P K A D A E W T G A L K A K V D G N K A K L A G K M T A E T P S G
CCAAAAGCTGACGCTGAATGGACCGGCGCTCTGAAAGCCAAAGTTGACGGCAACAAAGCCAAACTGGCTGGCAAGATGACTGCCGAAACCCCATCCGGAA
1121
1220
M M N Y S N S L G V V R D F M L A N P D I S L V N E G A N A L D N T
TGATGAACTACTCCAATTCCCTGGGCGTTGTTCGTGACTTCATGCTGGCAAATCCGGATATTTCCCTGGTTAACGAAGGCGCTAATGCACTCGACAACAC
1221
1320
R M I V D M L K P R K R L D S G T W G V M G I G M G Y C V A A A A
TCGTATGATTGTTGACATGCTGAAACCACGCAAACGTCTTGACTCCGGTACCTGGGGTGTTATGGGTATTGGTATGGGCTACTGCGTTGCTGCAGCTGCT
1321
[----------TPP Binding Motif----------
1420
V T G K P V I A V E G D S A F G F S G M E L E T I C R Y N L P V T
GTTACCGGCAAACCGGTTATCGCTGTTGAAGGCGATAGCGCATTCGGTTTCTCCGGTATGGAACTGGAAACCATCTGCCGTTACAACCTGCCAGTTACCG
1421 ----------]
1520
V I I M N N G G I Y K G N E A D P Q P G V I S C T R L T R G R Y D M
TTATCATCATGAACAATGGTGGTATCTATAAAGGTAACGAAGCAGATCCACAACCAGGCGTTATCTCCTGTACCCGTCTGACCCGTGGTCGTTACGACAT
1521
1620
M M E A F G G K G Y V A N T P A E L K A A L E E A V A S G K P C L
GATGATGGAAGCATTTGGCGGTAAAGGTTATGTTGCCAATACTCCAGCAGAACTGAAAGCTGCTCTGGAAGAAGCTGTTGCTTCCGGCAAACCATGCCTG
1621
1705
1720
I N A M I D P D A G V G S G R I K S L N V V S K V G K K
ATCAACGCGATGATCGATCCAGACGCTGGTGTCGAATCTGGCCGTATCAAGAGCCTGAACGTTGTAAGTAAAGTTGGCAAGAAATAATTAGCCCAACTTT
1721
1758
1820
GATGACCGGTTACGACCGGTCACATAAAGTGTTCGAATGCCCTTCAAGTTTACTTGAAGGGCATTTTTTTACCTTGCAGTTTATAAACAGGAAAAATTGT
1821
1908
ATTCAGAGCGGAAAAGCAGATTTAAGCCACGAGAAACATTCTTTTTTATTGAAAATTGCCATAAACACATTTTTAAAGCTGGCTTTTT

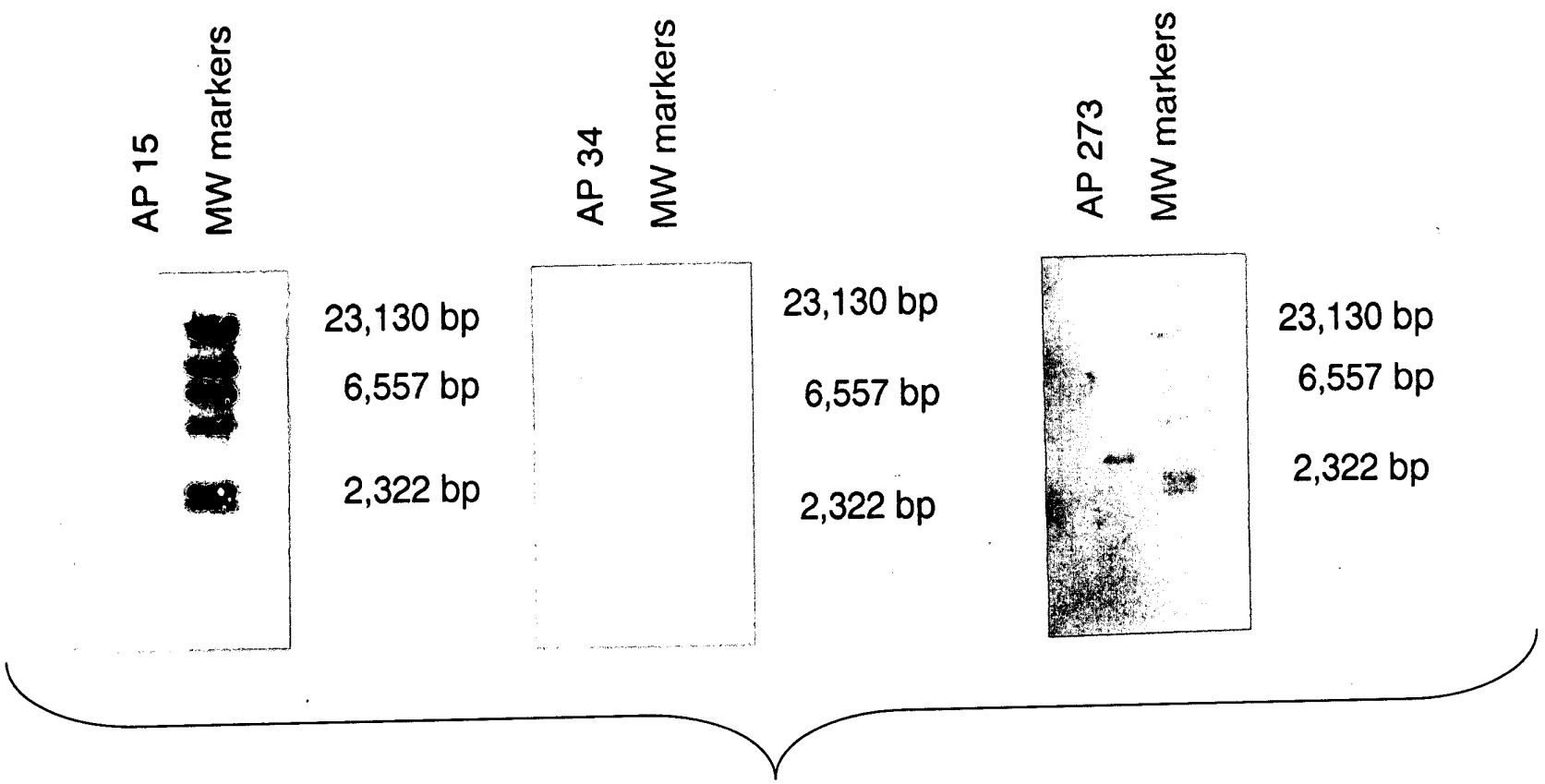

AP 15
MW markers
23,130 bp
6,557 bp
2,322 bp
AP 34
MW markers
23,130 bp
6,557 bp
2,322 bp
AP 273
MW markers
23,130 bp
6,557 bp
2,322 bp

FIG. 4

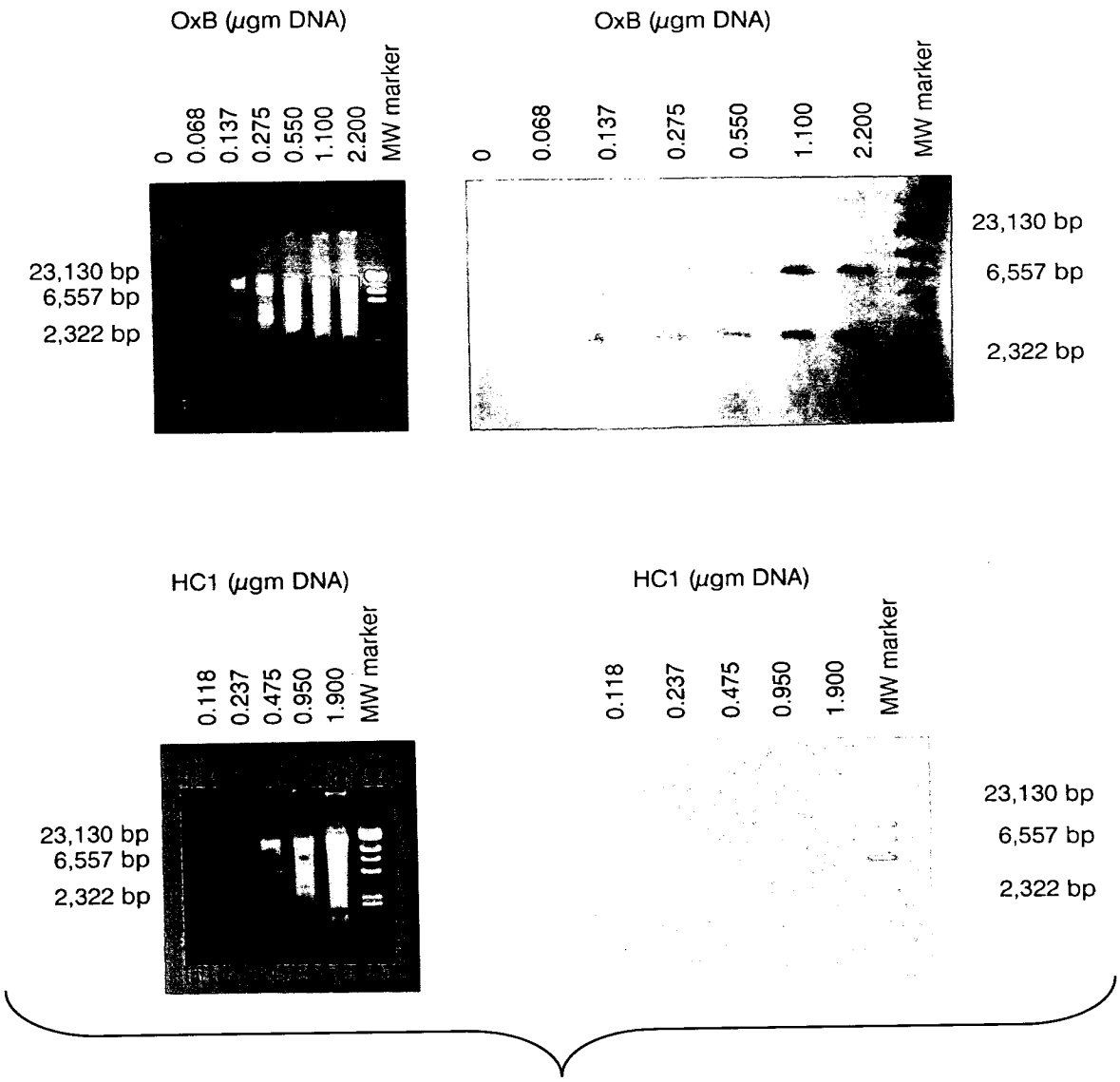

OxB (μgm DNA)
0
0.068
0.137
0.275
0.550
1.100
2.200
MW marker
23,130 bp
6,557 bp
2,322 bp
OxB (μgm DNA)
0
0.068
0.137
0.275
0.550
1.100
2.200
MW marker
23,130 bp
6,557 bp
2,322 bp
HC1 (μgm DNA)
0.118
0.237
0.475
0.950
1.900
MW marker
23,130 bp
6,557 bp
2,322 bp
HC1 (μgm DNA)
0.118
0.237
0.475
0.950
1.900
MW marker
23,130 bp
6,557 bp
2,322 bp

FIG. 5

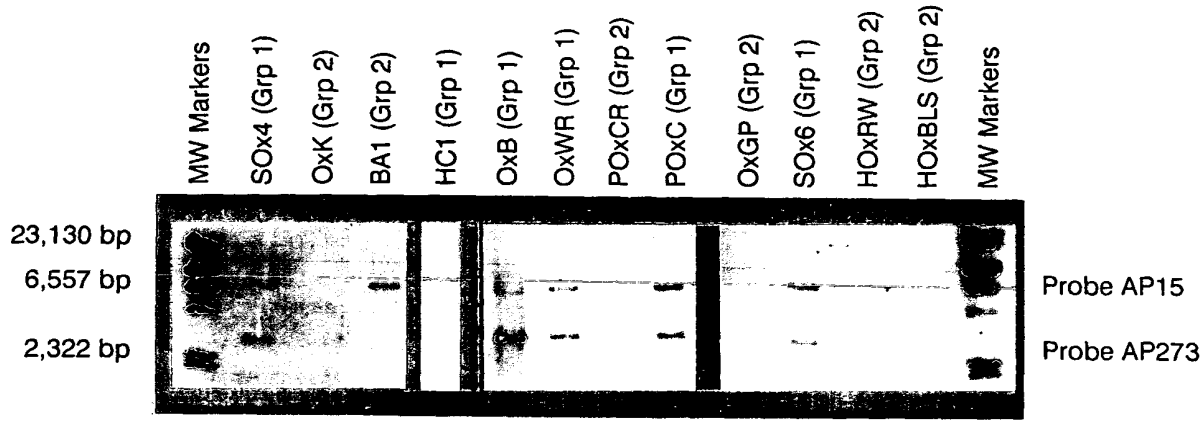


FIG. 6

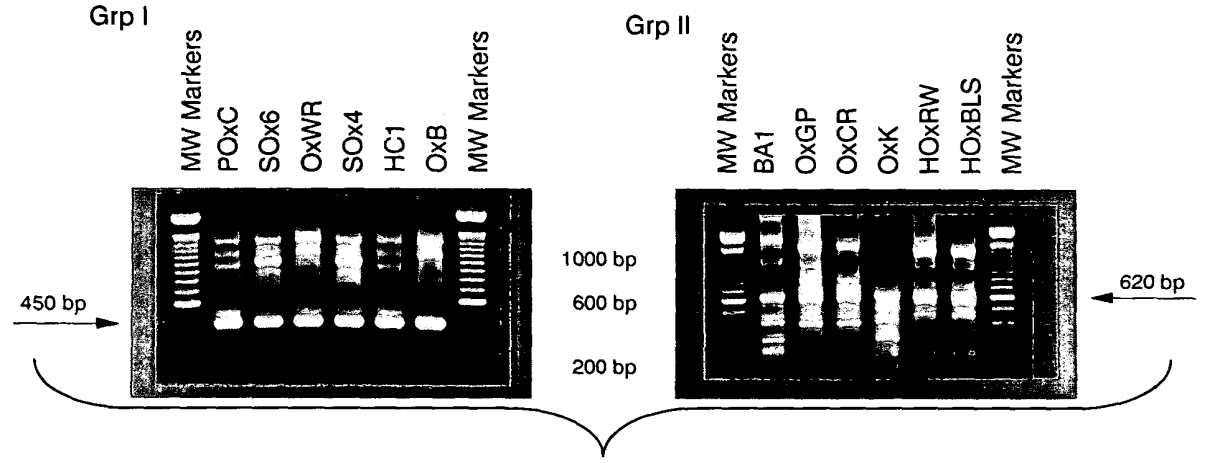


FIG. 7

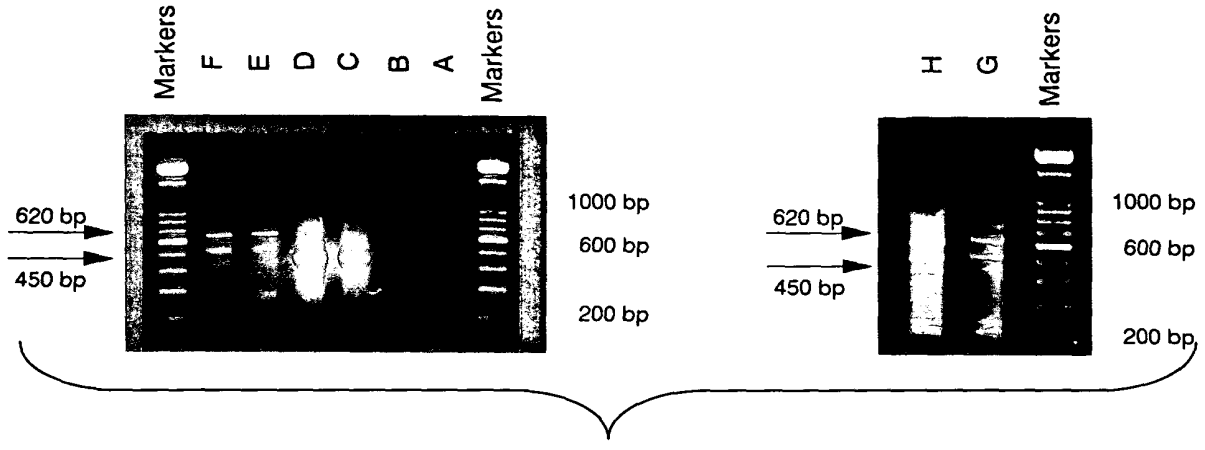


FIG. 8

FIG. 9A

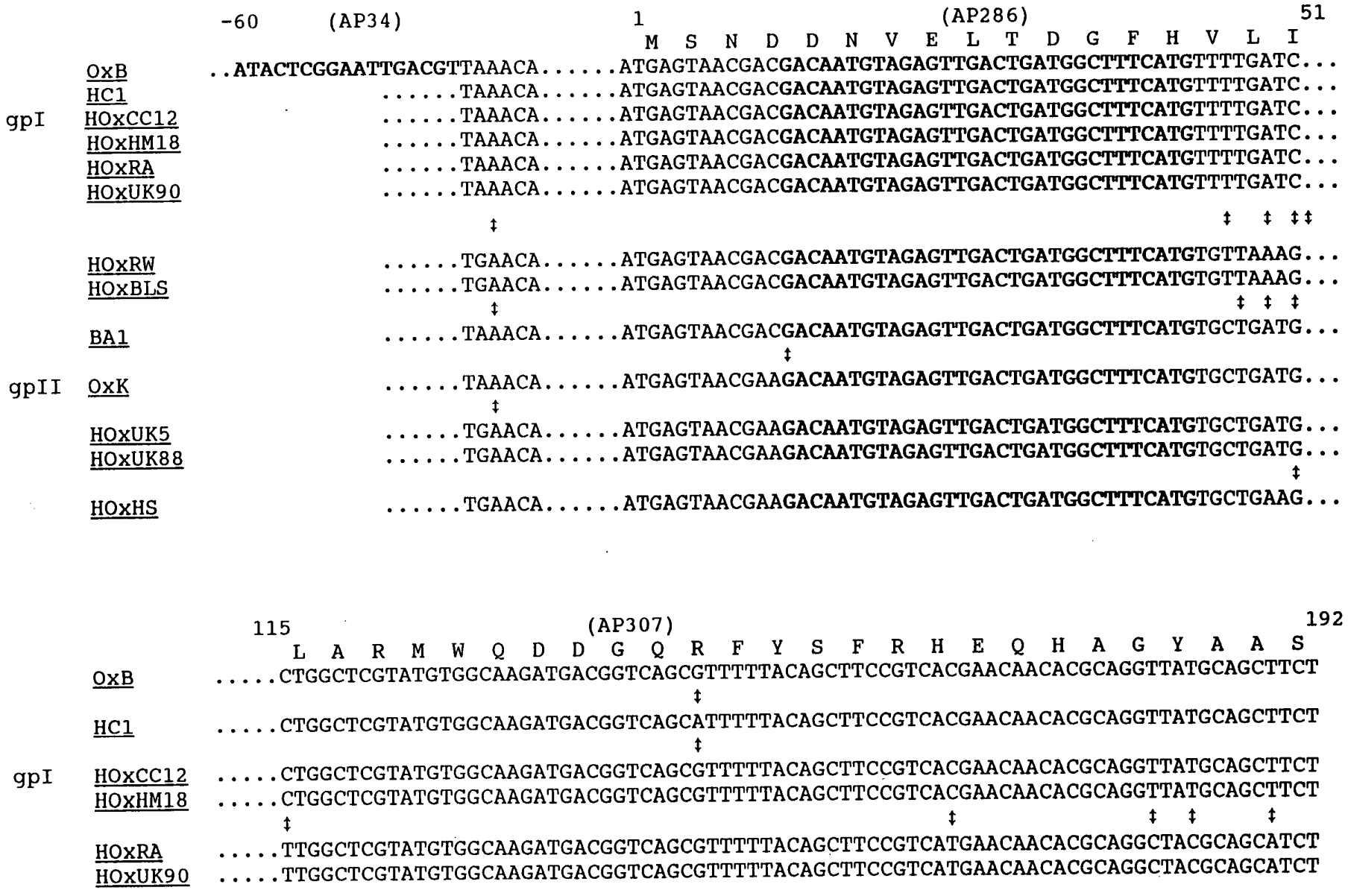

-60
(AP34)
1
(AP286)
51
M S N D D N V E L T D G F H V L I
OxB ..ATACTCGGAATTGACGTTAAACA.....ATGAGTAACGACGACAATGTAGAGTTGACTGATGGCTTTCATGTTTTGATC...
HC1 .....TAAACA.....ATGAGTAACGACGACAATGTAGAGTTGACTGATGGCTTTCATGTTTTGATC...
gpI HOxCC12 .....TAAACA.....ATGAGTAACGACGACAATGTAGAGTTGACTGATGGCTTTCATGTTTTGATC...
HOxHM18 .....TAAACA.....ATGAGTAACGACGACAATGTAGAGTTGACTGATGGCTTTCATGTTTTGATC...
HOxRA .....TAAACA.....ATGAGTAACGACGACAATGTAGAGTTGACTGATGGCTTTCATGTTTTGATC...
HOxUK90 .....TAAACA.....ATGAGTAACGACGACAATGTAGAGTTGACTGATGGCTTTCATGTTTTGATC...
HOxRW .....TGAACA.....ATGAGTAACGACGACAATGTAGAGTTGACTGATGGCTTTCATGTGTTAAAG...
HOxBLS .....TGAACA.....ATGAGTAACGACGACAATGTAGAGTTGACTGATGGCTTTCATGTGTTAAAG...
BA1 .....TAAACA.....ATGAGTAACGACGACAATGTAGAGTTGACTGATGGCTTTCATGTGCTGATG...
gpII OxK .....TAAACA.....ATGAGTAACGAAGACAATGTAGAGTTGACTGATGGCTTTCATGTGCTGATG...
HOxUK5 .....TGAACA.....ATGAGTAACGAAGACAATGTAGAGTTGACTGATGGCTTTCATGTGCTGATG...
HOxUK88 .....TGAACA.....ATGAGTAACGAAGACAATGTAGAGTTGACTGATGGCTTTCATGTGCTGATG...
HOxHS .....TGAACA.....ATGAGTAACGAAGACAATGTAGAGTTGACTGATGGCTTTCATGTGCTGAAG...
115
(AP307)
192
L A R M W Q D D G Q R F Y S F R H E Q H A G Y A A S
OxB .....CTGGCTCGTATGTGGCAAGATGACGGTCAGCGTTTTTACAGCTTCCGTCACGAACAACACGCAGGTTATGCAGCTTCT
HC1 .....CTGGCTCGTATGTGGCAAGATGACGGTCAGCATTTTTACAGCTTCCGTCACGAACAACACGCAGGTTATGCAGCTTCT
gpI HOxCC12 .....CTGGCTCGTATGTGGCAAGATGACGGTCAGCGTTTTTACAGCTTCCGTCACGAACAACACGCAGGTTATGCAGCTTCT
HOxHM18 .....CTGGCTCGTATGTGGCAAGATGACGGTCAGCGTTTTTACAGCTTCCGTCACGAACAACACGCAGGTTATGCAGCTTCT
HOxRA .....TTGGCTCGTATGTGGCAAGATGACGGTCAGCGTTTTTACAGCTTCCGTCATGAACAACACGCAGGCTACGCAGCATCT
HOxUK90 .....TTGGCTCGTATGTGGCAAGATGACGGTCAGCGTTTTTACAGCTTCCGTCATGAACAACACGCAGGCTACGCAGCATCT

FIG. 9B

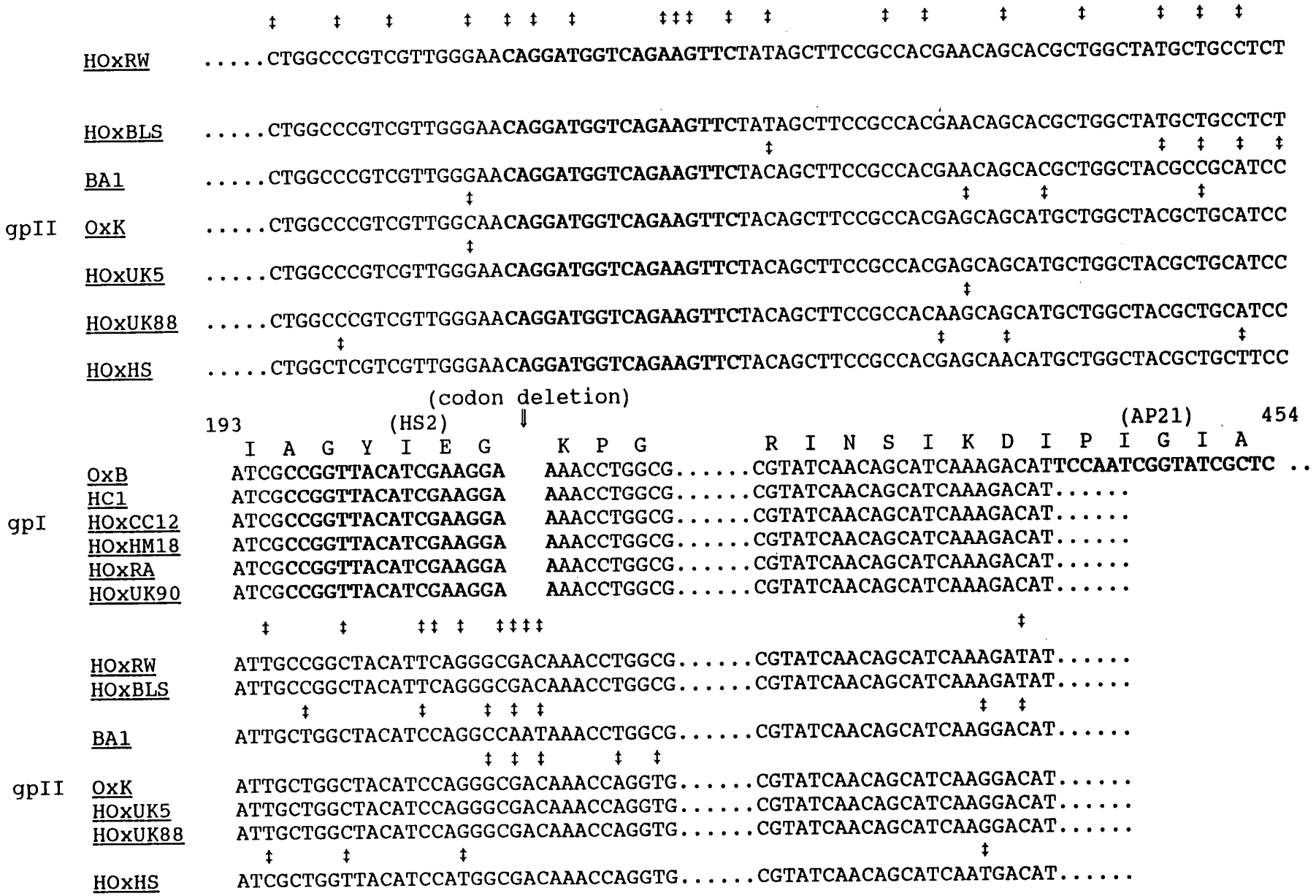

HOxRW .....CTGGCCCGTCGTTGGGAACAGGATGGTCAGAAGTTCTATAGCTTCCGCCACGAACAGCACGCTGGCTATGCTGCCTCT
HOxBLS .....CTGGCCCGTCGTTGGGAACAGGATGGTCAGAAGTTCTATAGCTTCCGCCACGAACAGCACGCTGGCTATGCTGCCTCT
BA1 .....CTGGCCCGTCGTTGGGAACAGGATGGTCAGAAGTTCTACAGCTTCCGCCACGAACAGCACGCTGGCTACGCCGCATCC
gpII OxK .....CTGGCCCGTCGTTGGCAACAGGATGGTCAGAAGTTCTACAGCTTCCGCCACGAGCAGCATGCTGGCTACGCTGCATCC
HOxUK5 .....CTGGCCCGTCGTTGGGAACAGGATGGTCAGAAGTTCTACAGCTTCCGCCACGAGCAGCATGCTGGCTACGCTGCATCC
HOxUK88 .....CTGGCCCGTCGTTGGGAACAGGATGGTCAGAAGTTCTACAGCTTCCGCCACAAGCAGCATGCTGGCTACGCTGCATCC
HOxHS .....CTGGCTCGTCGTTGGGAACAGGATGGTCAGAAGTTCTACAGCTTCCGCCACGAGCAACATGCTGGCTACGCTGCTTCC
(codon deletion)
193 (HS2) (AP21) 454
I A G Y I E G K P G R I N S I K D I P I G I A
OxB ATCGCCGGTTACATCGAAGGA AAACCTGGCG.....CGTATCAACAGCATCAAAGACATTCCAATCGGTATCGCTC ..
HC1 ATCGCCGGTTACATCGAAGGA AAACCTGGCG.....CGTATCAACAGCATCAAAGACAT.....
gpI HOxCC12 ATCGCCGGTTACATCGAAGGA AAACCTGGCG.....CGTATCAACAGCATCAAAGACAT.....
HOxHM18 ATCGCCGGTTACATCGAAGGA AAACCTGGCG.....CGTATCAACAGCATCAAAGACAT.....
HOxRA ATCGCCGGTTACATCGAAGGA AAACCTGGCG.....CGTATCAACAGCATCAAAGACAT.....
HOxUK90 ATCGCCGGTTACATCGAAGGA AAACCTGGCG.....CGTATCAACAGCATCAAAGACAT.....
HOxRW ATTGCCGGCTACATTCAGGGCGACAAACCTGGCG.....CGTATCAACAGCATCAAAGATAT.....
HOxBLS ATTGCCGGCTACATTCAGGGCGACAAACCTGGCG.....CGTATCAACAGCATCAAAGATAT.....
BA1 ATTGCTGGCTACATCCAGGCCAATAAACCTGGCG.....CGTATCAACAGCATCAAGGACAT.....
gpII OxK ATTGCTGGCTACATCCAGGGCGACAAACCAGGTG.....CGTATCAACAGCATCAAGGACAT.....
HOxUK5 ATTGCTGGCTACATCCAGGGCGACAAACCAGGTG.....CGTATCAACAGCATCAAGGACAT.....
HOxUK88 ATTGCTGGCTACATCCAGGGCGACAAACCAGGTG.....CGTATCAACAGCATCAAGGACAT.....
HOxHS ATCGCTGGTTACATCCATGGCGACAAACCAGGTG.....CGTATCAACAGCATCAATGACAT.....

FIG. 10A

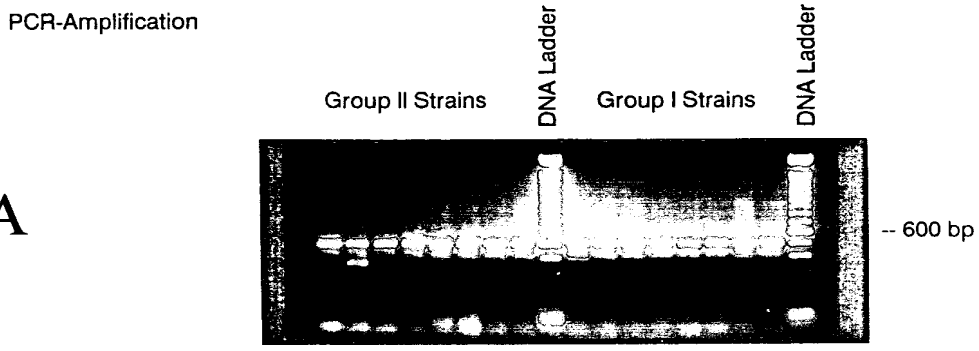
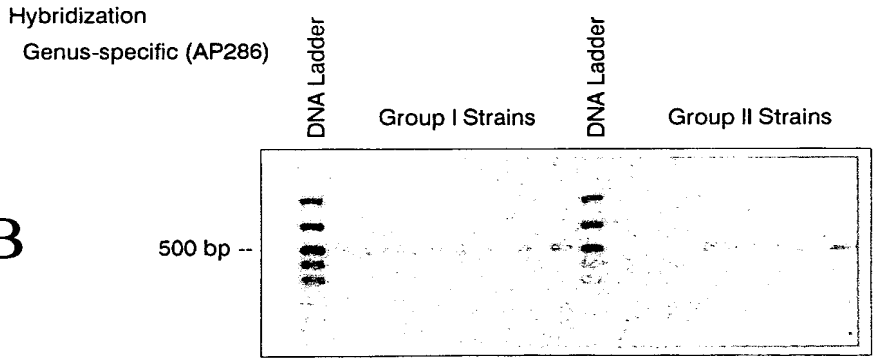
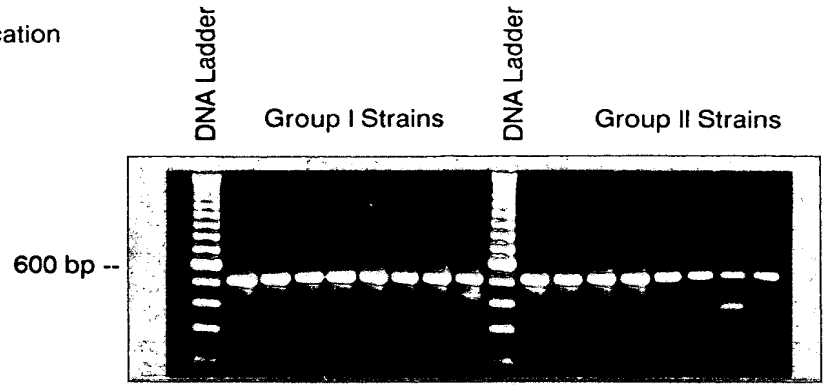


FIG. 10B



PCR-Amplification

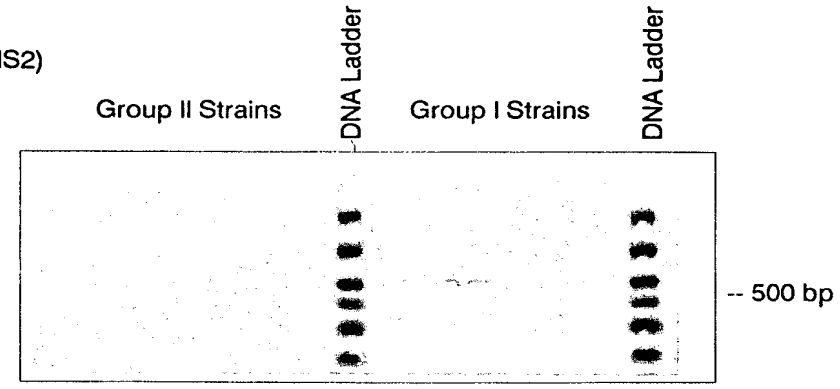
FIG. 11A



Hybridizations

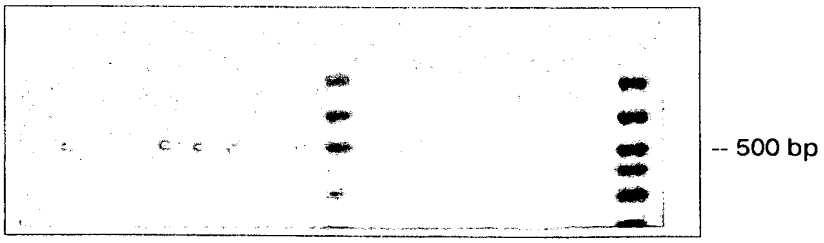
Group I-specific (HS2)

FIG. 11B



Group II-specific (AP307)

FIG. 11C



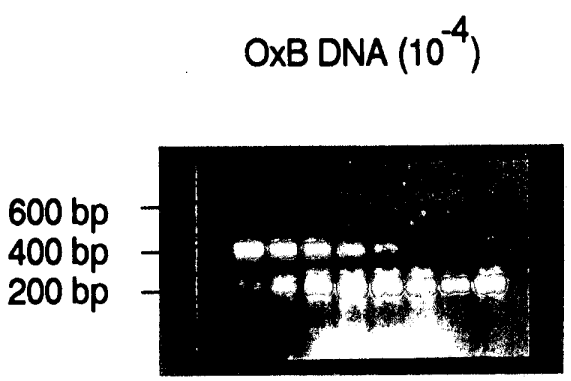


FIG. 12A

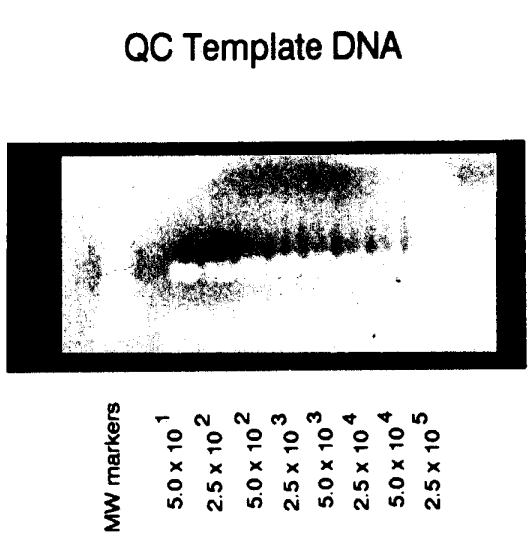


FIG. 12B

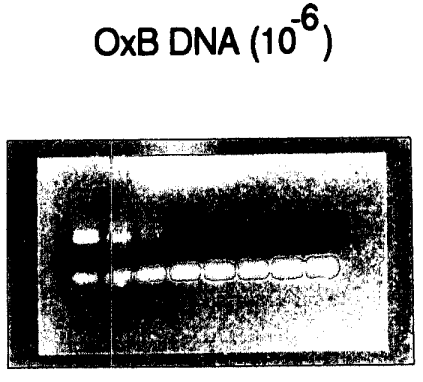
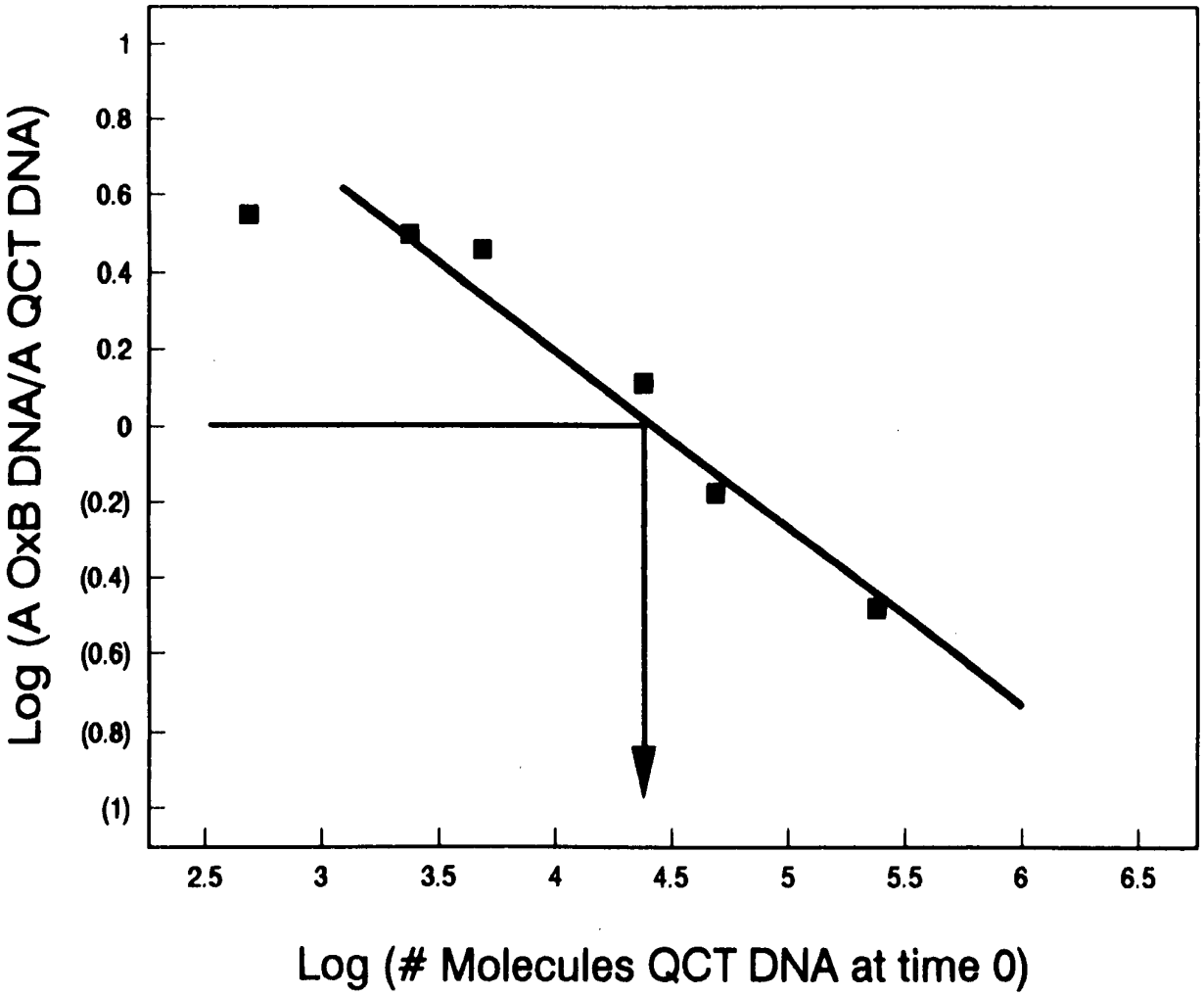


FIG. 12C

FIG. 12D


Log (A OxB DNA/A QCT DNA)
1
0.8
0.6
0.4
0.2
0
(0.2)
(0.4)
(0.6)
(0.8)
(1)
2.5
3
3.5
4
4.5
5
5.5
6
6.5
Log (# Molecules QCT DNA at time 0)

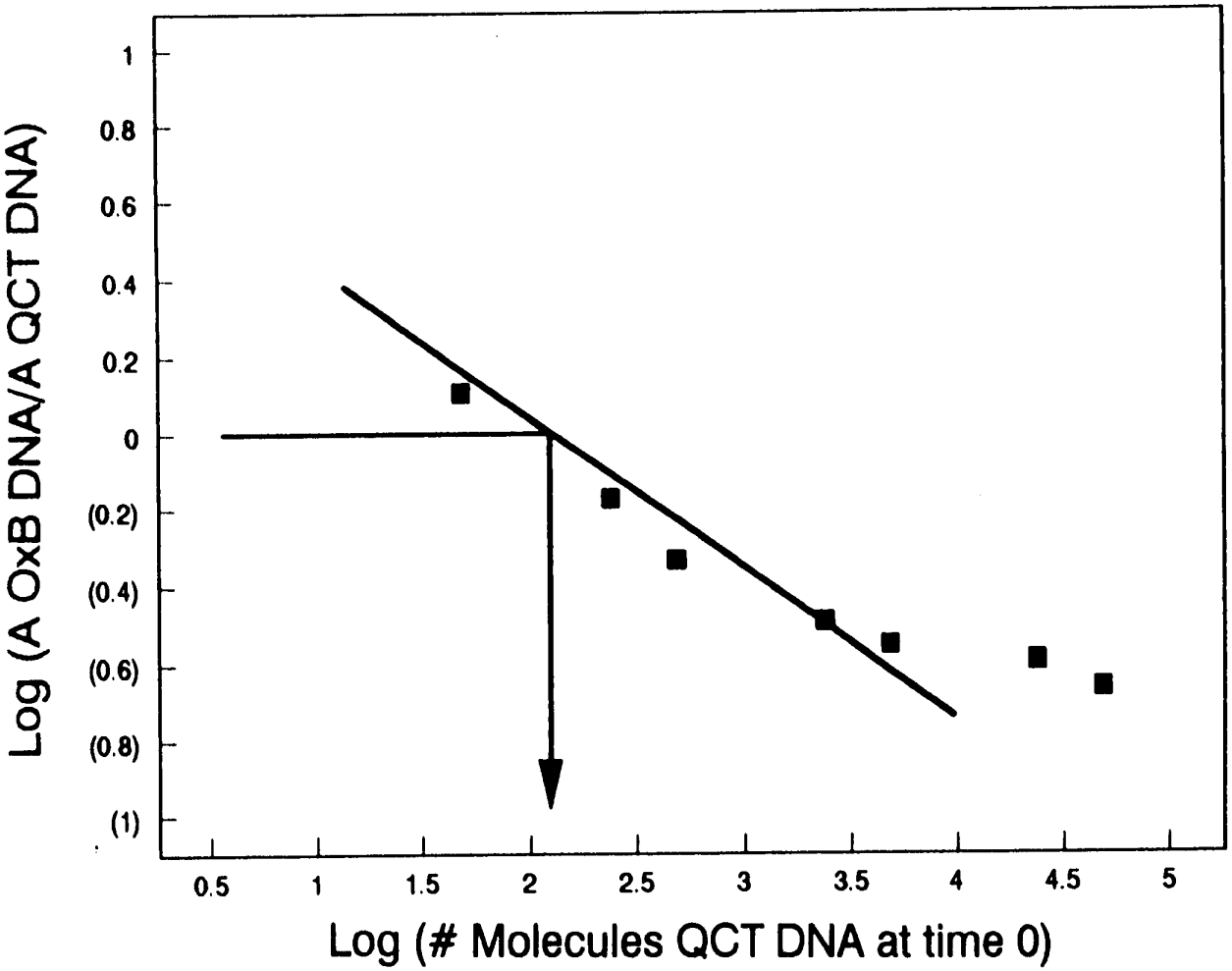

Log (A OxB DNA/A QCT DNA)
1
0.8
0.6
0.4
0.2
0
(0.2)
(0.4)
(0.6)
(0.8)
(1)
0.5
1
1.5
2
2.5
3
3.5
4
4.5
5
Log (# Molecules QCT DNA at time 0)

FIG. 12E